

AMENDMENTS TO THE CLAIMS:

Claims 21-40 are canceled without prejudice or disclaimer. Claims 1-20 were previously cancelled. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-20 (Canceled)

Claim 41 (New) A variant of an alpha-amylase having at least 90% homology to SEQ ID NO:8, comprising an alteration at a position corresponding to position 170 in SEQ ID NO:8, wherein the variant has alpha-amylase activity.

Claim 42 (New) The variant of claim 41, which variant comprises an alteration at one or more positions selected from the group of: 49, 60, 104, 132, 161, 176, 179, 180, 181, 183, 200, 203, 204, 207, 212, 237, 239, 250, 280, 298, 318, 374, 385, 393, 402, 406, 427, 430, 440, 444, 447, 482 (using SEQ ID NO:8 for numbering).

Claim 43 (New) The variant of claim 41, which variant comprises an alteration of K170Q.

Claim 44. (New) The variant of claim 41, which variant comprises an alteration of one or more of the following mutations: T49I; D60N; N104D; E132A,V,P; D161N; K170Q; K176R; G179N; K180T; A181N; D183N; D200N; X203Y; D204S; D207V,E,L,G; X212I; K237P; S239W; E250G,F; N280S; X298Q; L318M; Q374R; E385V; Q393R; Y402F; H406L,W; L427I D430N; V440A; N444R,K; E447Q,K; Q482K using SEQ ID NO: 8 for the numbering.

Claim 45 (New) The variant of claim 41, wherein the variant has the following mutations:
K170Q+D207V+N280S;
E132A+D207V;
D207E+E250G+H406L+L427I;
D207V+L318M;
D60N+D207V+L318M;
T49I+E132V+V440A;
T49I+K176R+D207V+Y402F;
Q374R+E385V+Q393R;

N190F+A209V+Q264S;
G48A+T49I+G107A+I201F;
T49I+G107A+I201F;
G48A+T49I+I201F;
G48A+T49I+G107A;
T49I+I201F; T49I+G107A; G48A+T49I;
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D4
30N+N444K+E447Q+Q482K;
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N4
44K+E447Q+Q482K;
D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+N444K+E447Q+Q4
82K;
D161N+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D430N+E447Q+Q482K;
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+D4
30N+E447Q+Q482K;
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+
D430N+E447Q+Q482K;
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+
H406W+D430N;
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+
D430N;
H406W+D430N; N444K+E447Q+Q482K; E447Q+Q482K;
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+
H406W+D430N+N444R+N444K+E447K+Q482K;
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W+H406W+
D430N+N444R+N444K+E447K+Q482K;
N104D+D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;
D161N+G179N+K180T+A181N+D183N+D200N+D204S+K237P+S239W;
H406W+D430N; N444K+E447K+Q482K; E447K+Q482K;
N104D+D161N+A181N+D183N+D200N+D204S+K237P+S239W;
N104D+D161N+A181N+D183N+D200N+D204S+K237P;
N104D+D161N+A181N+D183N+D200N+D204S;

D161N+A181N+D183N+D200N+D204S+K237P+S239W;

D161N+A181N+D183N+D200N+D204S+K237P;

D161N+A181N+D183N+D200N+D204S; K237P+S239W, using SEQ ID NO: 8 for the numbering.

Claim 46 (New) The variant of claim 41, wherein the variant is derived from a strain of *B. licheniformis*.

Claim 47 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 95%.

Claim 48 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 97%.

Claim 49 (New) The variant of claim 41, wherein the variant has an amino acid sequence which has a degree of homology to SEQ ID NO: 8 of at least 99%.

Claim 50 (New) The variant of claim 41, wherein the variant consists of an alteration at a position corresponding to position 170 in SEQ ID NO:8.